

**FIG. 1A-1**

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801 GACTCTCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCCGG GACTCTCTGCC  
 CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGGTGGTGG GGGCCCTGAG GACGGGGTGG ACGACTTCTC TGTTACTGGT GGTGGGGCCC CTGAGGACGG  
 204 ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGl yThrProAla  
 901 TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTAATTGT GCTTCTGATT GTGTTTGTTF GAAAGACTTC ACTGTGGAAG AAATTCCTTC  
 AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCCTAGTATC AAGATTAAAC CGAAGACTAA CACAAACAAA CTTTCTGAAG TGACACCTTC TTTAAGGAAG  
 237 SerSerHist yrLeuSerCy sThrIleVal GlyIleIlev alLeuIleVa lLeuLeuIle ValPheVal  
 1001 CTTACCTGAA AGGTTCAAGT AGGCGCTGGC TGAGGGGGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC AGAAACGCCT  
 GAATGGACTT TCCAAGTCCA TCCGGGACCG ACTCCGGCCC CCGCGACCT GTGAGAGACG GGACGGAGGG AGACGACACA AGGGTGTCTG TCTTTGCGGA  
 1101 GCCCTGCC CAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA  
 CCGGGACGGG GTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

# FIG.\_1A-2

1 GCTGTGGGAA CCTCTCCAG CGCAGCAACT CAGCCAAACGA TTCTGTATAG ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC  
 CGACACCCCTT GGAGAGGTGC GCGTGCCTGA GTCGGTTGCT TAAACACTATC AAAGACTATC TAAACACCT CAAACTGGTC TCTACGTTCC CCACTTCCTC GCGAAGGATG  
 MetGlnGl yValLysGlu ArgPheLeuPro

-40

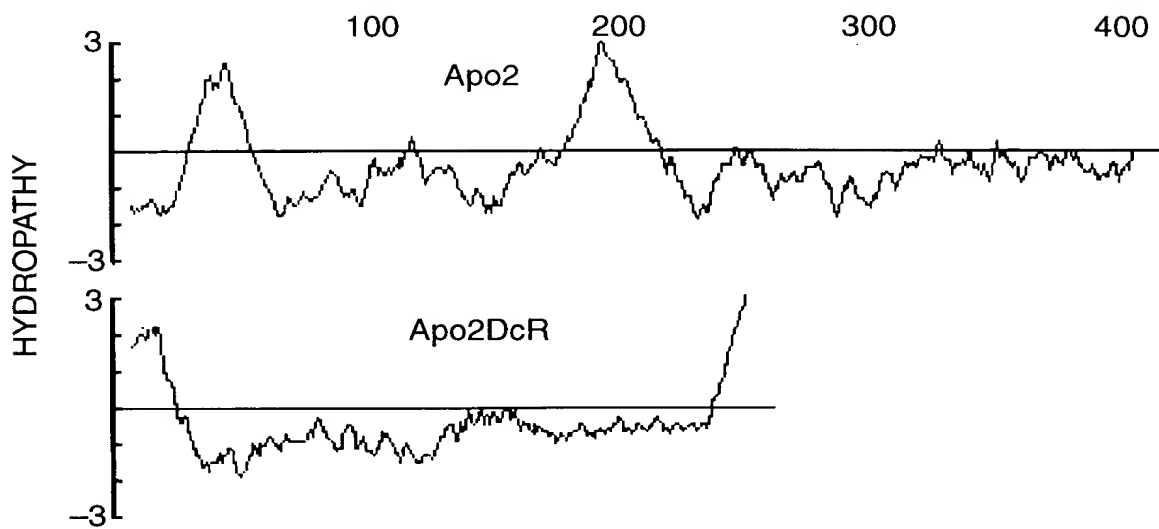
101 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GCGCGCCTGA TGGCCGAGGC AGGGTGGAC CCAGGACCCA GGACGGCGTC GGAACCATA CCATGGCCCCG  
 GCAATCCCTT GAGACCCCTG TCTCGCGGGG CCGGCGGACT ACGGCTCCG TCCCACGCTG GGTCTGGGT CCTGCCGAG CCCTTGGTAT GGTACCGGGC  
 -30 LeuGlyAs nSerGlyasp ArgAlaProA rgProProAs pGlyArgGly ArgValArgP roArgThrGl nAspGlyVal GlyAsnHist hrMetAlaArg  
 201 GATCCCCAAG ACCCTAAAGT TCGTCTCGT CATCGTCGGC GTCTGTCTGC CAGTCCTAGC TTACTCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG  
 CTAGGGGTC TGGGATTCA AGCAGCAGCA GTAGCAGCG CAGGACGACG GTCAGGATCG AATGAGACGG TGGTACGGG CCGTCTCTCT TCAAGGGGTC  
 4 IleProLys ThrLeuLysP heValValVa lIleValAla ValLeuLeuP roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluGl uValProGln  
 301 CAGACAGTGG CCCCACAGCA ACAGAGGCAC AGCTTCAAG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAAACATAC TGGAGCCTGT AACCCGTGCA  
 GTCTGTACCC GGGGTGCTG TGCTCCCGT TCGAAGTTCC CCGTCTCTAC AGGTCTCTCT ACAGTATCTA GTCTTGTATG ACCTGGGACA TTGGGCACGT  
 37 GlnThrVala laProGlnGl nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCys AsnProCysThr

# FIG.\_1B-1

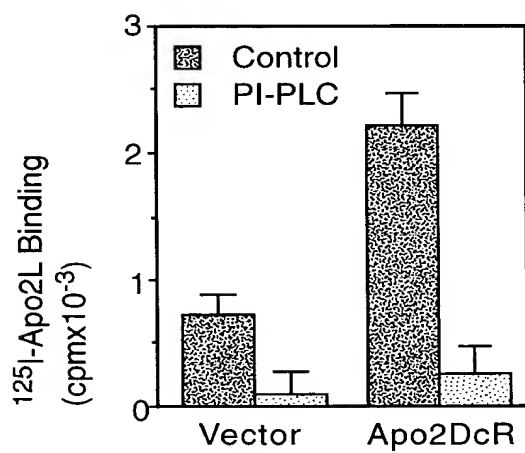


Apo2	1	-----MEQRGQNAFAASGARKRHGPGPREARGARPGLRVPKTLVL
Apo2DcR	1	-----MARIPKTLKFVV
DR4	51	GRGALPTSMGQHGPSARARAGRAPHRPAREASPRLRVHKTFKFVVVGVL
Apo2	41	VVAAVLLLVSAESALITQODLAPQORAAPOQKRSSPSEGLCPPGHHISED
Apo2DcR	13	VIVAVLLPVLAYSATTARQEEVPOQTVAPQQRHSFKGEECPAGSHRSEH
DR4	101	LQVVPSSAATIK-----LHDQSIGTQOWEHSPLGELCPPGSHRSEH
Apo2	91	GRDCISCKYGDYSTHWNDLLECLRCRDSGGEVELSPCTTTTRNTVCQCE
Apo2DcR	63	TGACNECTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTTRDTVCQCK
DR4	142	FGACNRCTEGVGYTNASNNLFACLPCTACKSDEEERSPCTTTTRNTACQCK
Apo2	141	EGTFREEDSPEMCRKCRGTGCPRGMVKVGDCPTWSDIECVHKE-----
Apo2DcR	113	EGTFRNENSPEMCRKCSR-CPSGEVQVSNCTSWDDIQVE-EFGANATVE
DR4	192	FGTFRNENSAEMCRKCRGTGCPRGMVKVKDCTPWSIECVHKE-----
Apo2		-----
Apo2DcR	161	TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
DR4		-----
Apo2	183	-----SGIIGVTVAAVVLIVAVEV---
Apo2DcR	211	ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV
DR4	234	-----SGNGHNIWVILVVTLVVPIILIVAV-LIVC
Apo2	203	CKSLLWKVLPYLKGICSGGGGDPERVDRSSQRPGAEDNVLNEIVSILQP
DR4	262	CCIGSGCGGDEPKCMDRVCFWRLGLLRGPGAEDNAHNEILSNADSLSTFVS
Apo2	253	TQVPEQEMEVOEPAEFTGVNMLSPGESEHLLPEAAERSORRRLLVPANE
DR4	312	----EQQMESQEPADLTGVTVQSPGEAQCLLGPAEAEGSORRRLLVPANG
Apo2	303	GDPTETLRQCFDDFADLVPFDSWEPLMRKLGIMDNEIKVAKAEAAGH--R
DR4	358	ADPTETLMLEFDKFAIVPFDSWDQLMRQLDITKNEIDVVRAGTAGP--G
Apo3/DR3	338	VMDAVPARRWKEFVRTLGLREAEIEAVEVEI-GRF-R
TNFR1	322	VVENVPPLRWKEFVRRGLSDHEIDRIELON-GRCLR
CD95	220	IAGVHTLSQVKGFRKNGVNEAKIDEIKNDN-VQDTA
Apo2	351	DILYTMLIKWVNKTGR-DASVHTLLDAETLGERLAKOKIEDHLLSSGKF
DR4	406	DALYAMLMKWVNKTGR-NASHTLLDALERMERHAKKEKIQDLLVDSGKF
Apo3/DR3	374	DQQYEMLKRWRRQQP---AGLGAVYAALERMGLDGCVEDLRS
TNFR1	358	EAQYSMLATWRRRTERRREATLEILGRVLRDMDLLGCLEDIEE
CD95	256	EQKVQILRNWHQLHGKKEAY-DTLIKDLKKANLCTLAEKIQT
Apo2	400	MYLEGNADSALS
DR4	455	IYLEDGTGSAVSL

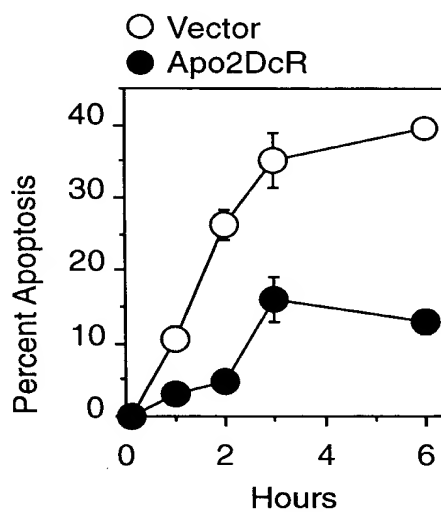
**FIG.\_2**



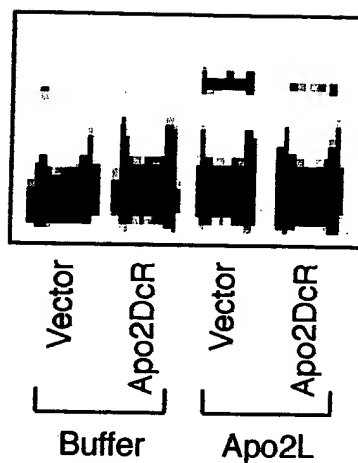
**FIG.\_3**



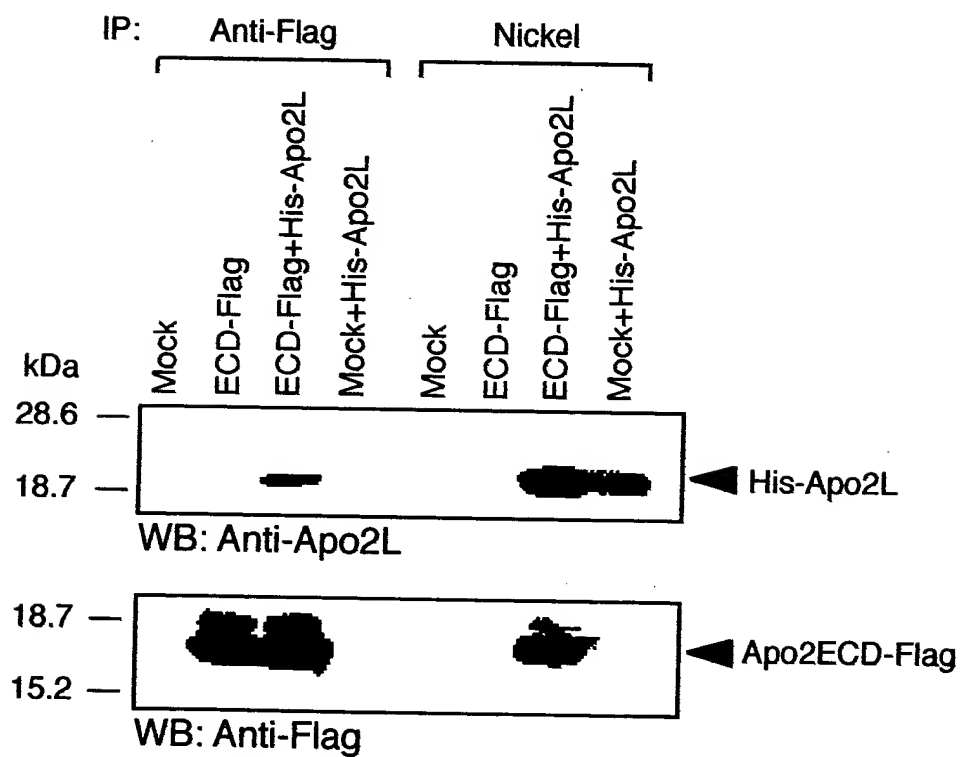
**FIG.\_4**



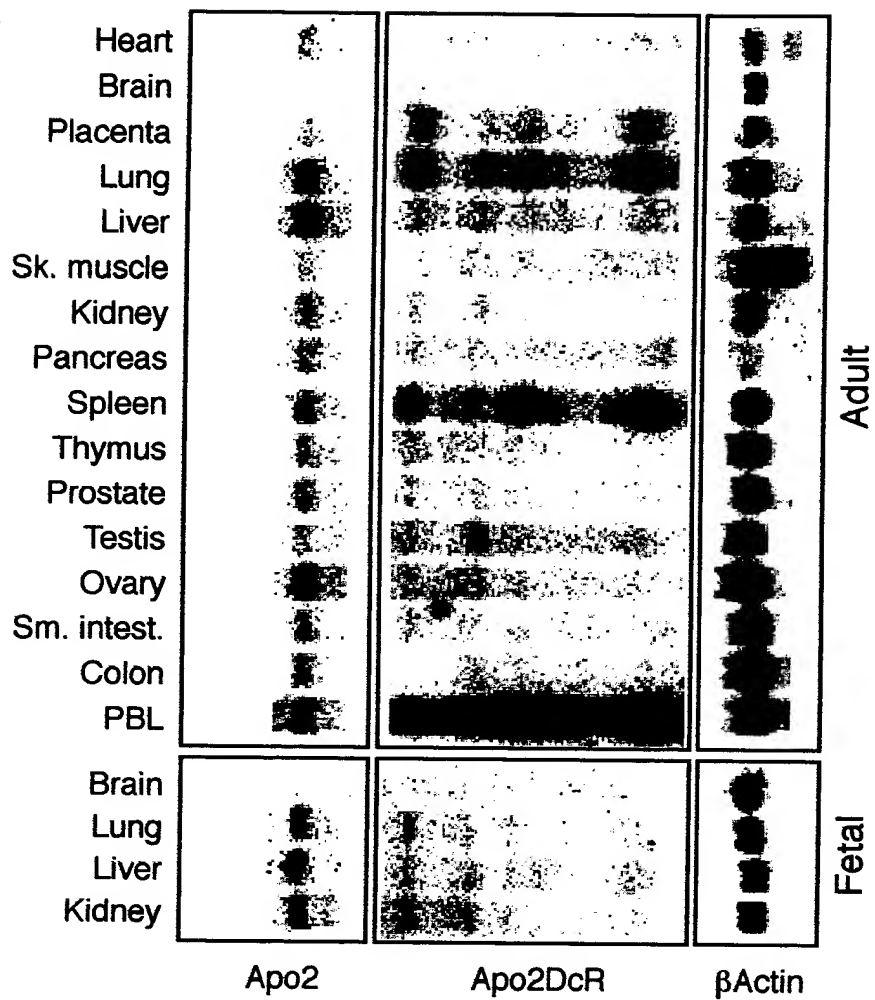
**FIG.\_5**



**FIG.\_6**



**FIG.\_10**



**FIG. 7**

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1 CCCACGGCTC GGCATRAATC AGCAGCGGGC CGGAGAAGCC CGCATATCTCT GCGCCACAAA AATACACCGA CGATGCCCCG TCTACTTTAA GGGCTGAAC  
GGGTGCGCAG CGGTATTAG TCGTGGCGCG CCTCTTGGG GCGTTAGAGA CCGGGGTCTT TTATGTGGCT CCTACGGGCT AGATGAAATT CCGGACTTTG

101 CCACGGGCTT GAGAGACTAT AAGAGCGTTC CCTACCGCCA TGGACAACG GGGACAGAAC GCGCCGGCGG CTTCGGGGGG CCGGAAAAGG CACGGGCCAG  
GGTCCCGGA CTCCTGATA TTCTCGCAAG GGATGGCGGT ACCTTGTCG CCTGTCTTG CCGGGCGCGG GAAGCCCCCG GGCCTTTTCC GTGCGGGGTC

1 M etGluGlnAr gGlyGlnAsn AlaProAlaI aSerGlyAl aArgLysArg HisGlyProGly

201 GACCCAGGGA GCGCGGGGA GCGAGGCGCTG GGCTCCGGGT CCCCAAGACC CTGTGCTCG TTGTGCGCGG GCTCCTGCTG TTGGTCTCAG CTGACTCTGC  
CTGGGTCCCT CCGCGCCCT CCGTCCGGAC CCGAGGCCCA GGGGTTCTGG GAACACGAGC AACAGCGGGC CACGAGCGAC AACAGAGTC GACTCAGACG

22 ProArgG1 uAlaArgGly AlaArgProG lyLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValSera laGluSerAla

301 TCTGATCACC CAACAAGACC TAGCTCCCCA GCAGAGAGCG GCCCCACAAC AAAAGAGGTC CAGCCCTCA GAGGATTGT GTCCACCTGG ACACCATATC  
AGACTAGTGG GTTGTCTGG ATCGAGGGGT CGTCTCTCG CGGGTCTTG TTTTCTCCAG GTCGGGGAGT CTCCCTAACA CAGGTGGACC TGTGCTATAG

55 LeuileThr GlnGlnAspL euAlaProG1 nGlnArgAla AlaProGlnG lNlysArgSe rSerProSer GluGlyLeuC ysProProG1 yHisHisIle

401 TCAGAAAGACG GTAGAGATTG CATCTCCTGC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTTCTGCTT GCGCTGCACC AGGTCTGATT  
AGTCTTCTGC CATCTCTAAC GTAGAGGACG TTTATACCTG TCCTGATATC GTGAGTGACC TTACTGGAGG AAAAGACGAA CCGCAGCTGG TCCACACTAA

88 SerGluAspG lyArgAspCy sIleSerCys LysTyrglyG lNAspTyrSe rThrHisTriP AsnAspLeuL euPheCysLe uArgCysThr ArgCysAspSer

501 CAGGTGAAGT GGAGCTAAGT CCCTGCACCA CGACCAGAAA CACAGTGTGT CAGTGGCAG AGGCACCTT CCGGGAAGAA GATTCTCCTG AGATCTGCCG  
GTCCACTTCA CCTCGATTCA GGGACGTGGT GCTGGTCTTT GTGTACACA GTACCGTGA TCCCTTCTT CTAAGAGGAC TCTACACGGC

122 GlyGluVa lgluLeuSer ProCysThrT hrThrArgAs nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspSerProG luMetCysArg

601 GAAGTGCCGC ACAGGGTGTG CCAGAGGGAT GGTCAAAGTC CCGTATTGTA CACCCCTGGAG TGACATCGAA TGTGTCCACA AAGAATCAGG CATCATCATA  
CTTCACGGCG TGTCCACACG GGTCTCCCTA CCAGTTCCAG CCACTAACAT GTGGGACCTC ACTGTAGCTT ACACAGGTGT TTCTTAGTCC GTAGTAGTAT

155 LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyAspCysT hrProTriPse rAspIleGlu CysValHisL ysGluSerG1 yIleIleIle

701 GGAGTCACAG TTGCAGCCGT AGTCTTGATT GTGGCTGTGT TTCTTTGCAA GTCTTTACTG TGGAGAAGAG TCCTTCCTTA CCTGAAAGGC ATCTGCTCAG  
CCTCAGTCTC AACGTGGCA TCAGAACTAA CACCGACACA CACAAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC

188 GlyValThrV alAlaAlaVa lValLeuIle ValAlaValP heValCysLy sSerLeuLeu TriLysLysV alLeuProTy rLeuLysGly IleCysSerGly

FIG.\_8A-1





801 GTGGTGGTGG GGACCTGAG CGTGTGGACA GAAGCTCACA ACGACCTGGG GCTGAGGACA ATGTCTCTCAA TGAGATCGTG AGTATCTTGC AGCCACCCA  
 CACCACCACC CCTGGGACTC GCACACCTGT CTTCGAGTGT TGCTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT  
 222 GlyGlyGly YAspProGlu ArgValAspA rGSerSerG1 nArgProGly AlaGluAspA snValLeuAs nGluIleVal SerIleLeuG InProThrGln  
 901 GGTCCCTGAG CAGGAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA  
 CCAAGGACTC GTCCTTTACC TTCAGGTCCTT CCGTCGTCTC GGTGTGCCAC AGTTGTACAA CAGGGGGCCC CTCAGTCTCG TAGACGACCT TGGCCGTCTT  
 255 ValProGlu GlnGluMetG luValGlnG1 uProAlaGlu ProThrGlyV alaSnMetLe uSerProGly GluSerGluH isLeuLeuG1 uProAlaGlu  
 1001 GCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACCTGAG ACTCTGAGAC AGTGCTTCGA TGACTTTGCA GACTTGGTGC  
 CGACTTTCCA GAGTCTCCTC CTCGGACGAC CAAGGTGCTT TACTTCCACT AGGGTGACTC TGAGACTCTG TCACGAAAGCT ACTGAAACGT CTGAACCACG  
 288 AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG InCysPheAs pAspPheAla AspLeuValPro

**FIG. 8A-2**

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

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1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA ACTTGGGCCT CATGGACAAT GAGATAAAGG TGGCTAAAGC TGAGGCAGCG GGCCACAGGG ACACCTTGTA  
 GGAACACGAG GACCTCGGC GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCTATTCC ACCGATTTCG ACTCCGTCCG CCGGTGTCCT TGTGGAACAT  
 322 PheAspSe rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluileLysV alAlaLysAl aGluAlaAla GlyHisArgA spThrLeuTyr  
 1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCCCTGT GGATGCCTTG GAGACGCTGG GAGAGAGACT TGCCAAGCAG  
 GTGCTACGAC TATTTCACCC AGTTGTTTGG GCCGCTCTA CGGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGCGACC CTCTCTCTGA ACGGTTCGTC  
 355 ThrMetLeu IleLysTrpV alAsnLysTh rGlyArgasp AlaservAlH isThrLeule uAspAlaLeu GluThrLeug lyGluArgLe uAlaLysGln  
 1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT ATCTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA  
 TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGACGGAACA GGATTCACAC TAAGAGAAAGT CCTTCACACTCT  
 388 LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluGl yAsnAlaAsp SerAlaXq4S erOC\*  
 1401 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC  
 GGAAGGGACC AAATGGAAAA AAGACCTTTT TCGGCTTGAC CTGAGGTCAG TCATCCTTTC ACGGTCTTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG  
 1501 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAT  
 GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AAAATATTGG ACTTACACTA TTATTCCCTGT GATACCTTTA  
 1601 GTCGTGATCA TTCCGTTTGT GCGTACTTTG AGATTGTTT TGGGATGTCA TTGTTTTTTC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT  
 CAGACCTAGT AAGGCAACA CGCATGAAC TCTAAACCA ACCCTACAGT ACAAAGAGTG TCGTGAAAAA ATAGGATTAC ATTTACGAAA TAAATAAATA  
 1701 TTGGGGCTACA TTGTAAGATC CATCTACAA AAAAAAAAAA GGGGGCCGCG ACTCTACAGT CGACCTGCAG AAGCTTGCC GCCATGGCC  
 AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTTTT CCGCCGGCGC TGAGATCTCA GCTGGACGTC TTCGAACCGG CCGTACCGG

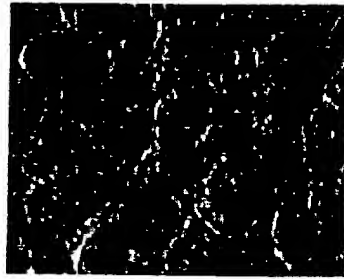
FIG.-8B

1 MEORGQNA PAASGARKRHGPGPREARGARPLRVKTLVLVVAAVLLLVSAESALITQQD  
 61 LAPQQRAAPQQKRSSPSEGLCPPGHHISEDGRDCISCKYQDYSTHWNDLLFCLRCTRCD  
 121 SGEVELSPCTTTRNTVCQEEGTFREEDSPEMCRKQRTGCPRGMVKVGDCPTWSDIECVH  
 181 KESGIIIGVTVAAVLIVAFVCKSLMKKVLPLYKIGICSGGGDPERVDRSSQRPGEAD  
 241 NVLNEIVSILQPTQVPEQEMEVQEPAEPTGVNMLSPGESEHLLLEPAEAERSQRRLLVPA  
 301 NEGDPTETLRQCFFDDFADLVFPDSEWELMRKLGMDNEIKVAKAEAAAGHRDTLYTMLIKW  
 361 VNKTGRDASVHTLLDALETGLERLAKQKIEDHLLSSGKFMYLEGNADSALS

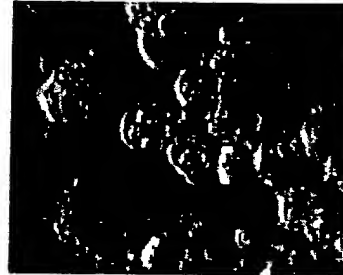
FIG.-9

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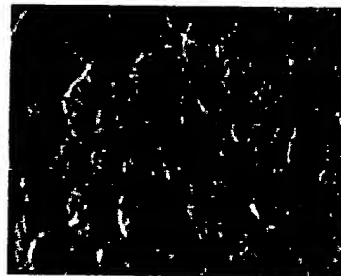
Vector



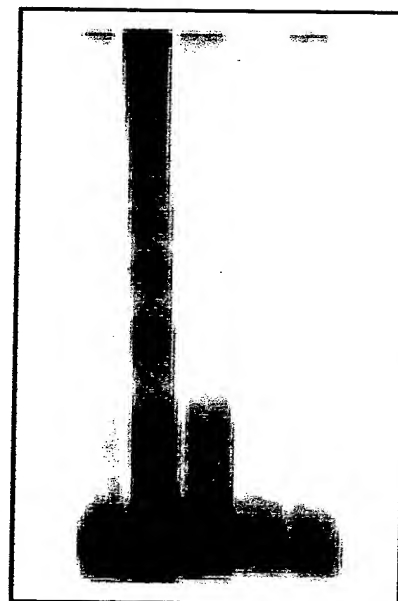
Apo2



Apo2+CrmA



**FIG.\_11A**



Vector

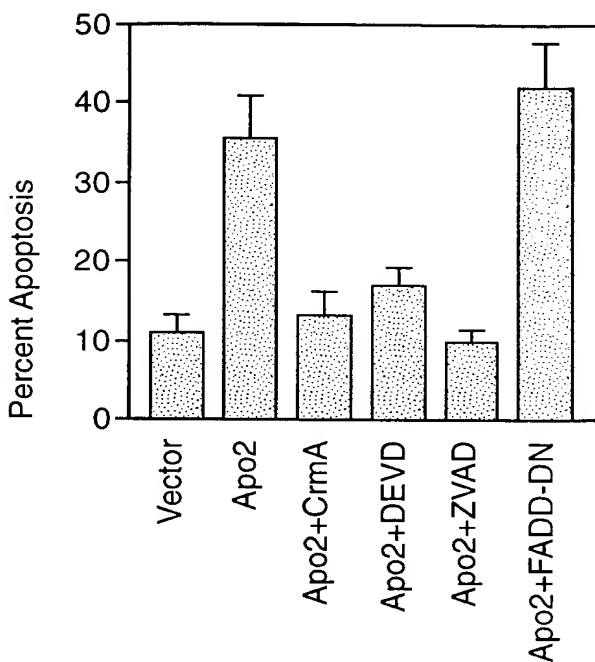
Apo2

Apo2+CrmA

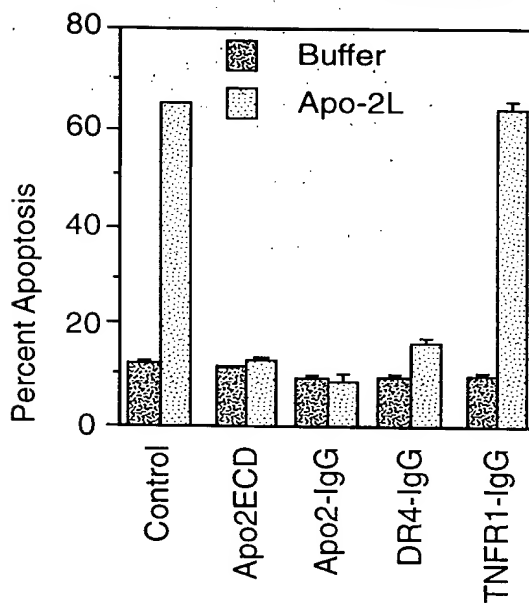
Apo2+DEVD

Apo2+ZVAD

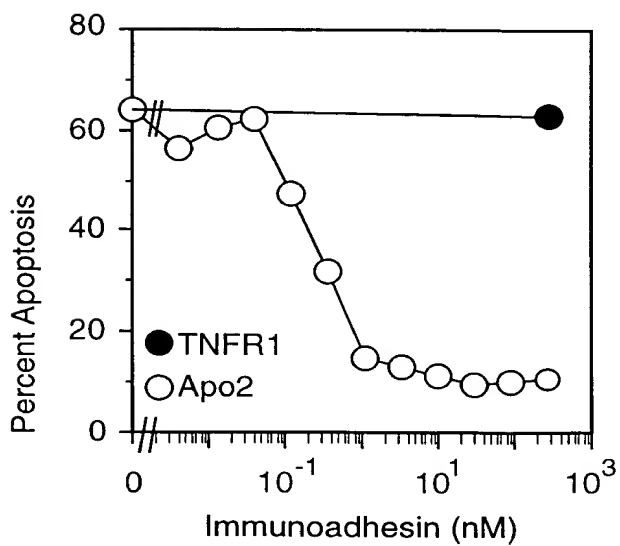
**FIG.\_11B**



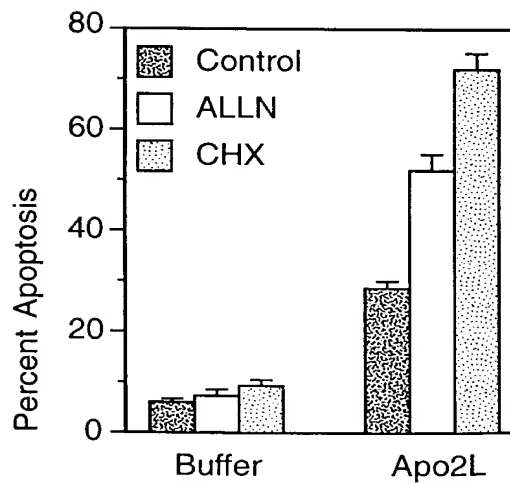
**FIG.\_11C**



**FIG.\_11D**



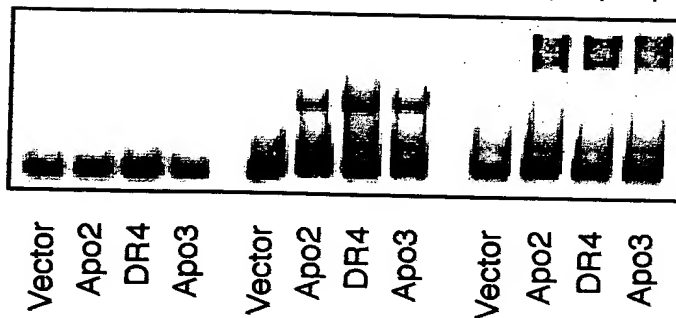
**FIG.\_11E**



**FIG.\_12C**

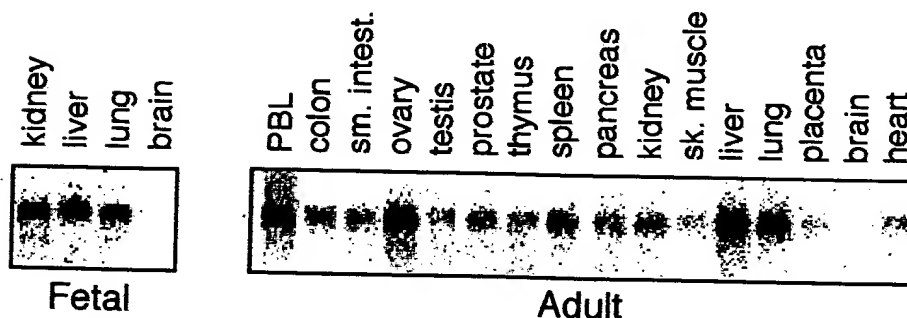
Unlabelled probe	+	+	+	+	-	-	-	-	-	-	-	-
Labelled probe	+	+	+	+	+	+	+	+	+	+	+	+
Anti-p65	-	-	-	-	-	-	-	-	+	+	+	+

**FIG.\_12A**



Unlabelled probe	-	-	-	-	-	-	-
Labelled probe	+	+	+	+	+	+	+
Anti-p65	-	-	-	-	-	-	-

**FIG.\_12B**



**FIG.\_13**